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SEQUENCE LISTING

<110> VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
DIJKHUIZEN, LUBBERT
RAHAOUI, HAKIM
LEER, ROBERT-JAN

<120> NOVEL GLUCOSYLTRANSFERASES

<130> BO43388-CIP

<140> 09/995,749

<141> 2001-11-29

<150> 09/604,957

<151> 2000-06-28

<150> EPO 00201871.1

<151> 2000-05-25

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<170> PatentIn Ver. 2.1

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Gly Trp Asn Ala Thr Asn Ala Ser Gln Gly Thr Asn Ser Arg Gln Ile
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Lys Asn Asn Tyr Ala Tyr Leu Asp Thr Phe Glu Val Lys Asn Gly Glu
 245 250 255

Leu His Ala Thr Gly Trp Asn Ala Thr Asn Ser Ala Ile Asn Tyr Asn
 260 265 270

His His Phe Val Ile Leu Phe Asp Gln Thr Asn Gly Lys Glu Val Ala
 275 280 285

Arg Gln Glu Val Arg Glu Gly Gln Ser Arg Pro Asp Val Ala Lys Val
 290 295 300
 Tyr Pro Gln Val Val Gly Ala Ala Asn Ser Gly Phe Asn Val Thr Phe
 305 310 315 320
 Asn Ile Ser Asp Leu Asp Tyr Thr His Gln Tyr Gln Val Leu Ser Arg
 325 330 335
 Tyr Ser Asn Ser Asp Asn Gly Glu Gly Asp Asn Val Thr Tyr Trp Phe
 340 345 350
 Asn Pro Gln Ser Ile Ala Pro Ala Asn Gln Ser Asn Gln Gly Tyr Leu
 355 360 365
 Asp Ser Phe Asp Ile Ser Lys Asn Gly Glu Val Thr Val Thr Gly Trp
 370 375 380
 Asn Ala Thr Asp Leu Ser Glu Leu Gln Asn Asn His Tyr Val Ile Leu
 385 390 395 400
 Phe Asp Gln Thr Ala Gly Lys Gln Val Ala Ser Ala Lys Ala Asp Leu
 405 410 415
 Ile Ser Arg Pro Asp Val Ala Lys Ala Tyr Pro Thr Val Lys Thr Ala
 420 425 430
 Thr Asn Ser Gly Phe Lys Val Thr Phe Lys Val Asn Asn Leu Gln Pro
 435 440 445
 Gly His Gln Tyr Ser Val Val Ser Arg Phe Ser Ala Asp Glu Asn Gly
 450 455 460
 Asn Gly Asn Asp Lys Arg His Thr Asp Tyr Trp Phe Ser Pro Val Ile
 465 470 475 480
 Leu Asn Gln Thr Ala Ser Asn Ile Asp Thr Ile Thr Met Thr Ser Asn
 485 490 495
 Gly Leu His Ile Ala Gly Trp Met Ala Ser Asp Asn Ser Ile Asn Glu
 500 505 510
 Thr Thr Pro Tyr Ala Ile Ile Leu Asn Asn Gly Lys Glu Val Thr Arg
 515 520 525
 Gln Lys Met Ser Leu Thr Ala Arg Pro Asp Val Ala Ala Val Tyr Pro
 530 535 540
 Ser Leu Tyr Asn Ser Ala Val Ser Gly Phe Asp Thr Thr Ile Lys Leu
 545 550 555 560
 Thr Asn Asp Gln Tyr Gln Ala Leu Asn Gly Gln Leu Gln Val Leu Leu
 565 570 575
 Arg Phe Ser Lys Ala Ala Asp Gly Asn Pro Ser Gly Asp Asn Thr Val
 580 585 590

Thr Asp Gln Phe Ser Lys Asn Tyr Ala Thr Thr Gly Gly Asn Phe Asp
 595 600 605
 Tyr Val Lys Val Asn Gly Asn Gln Val Glu Phe Ser Gly Trp His Ala
 610 615 620
 Thr Asn Gln Ser Asn Asp Lys Asp Ser Gln Trp Ile Ile Val Leu Val
 625 630 635 640
 Asn Gly Lys Glu Val Lys Arg Gln Leu Val Asn Asp Thr Lys Glu Gly
 645 650 655
 Ala Ala Gly Phe Asn Arg Asn Asp Val Tyr Lys Val Asn Pro Ala Ile
 660 665 670
 Glu Asn Ser Ser Met Ser Gly Phe Gln Gly Ile Ile Thr Leu Pro Val
 675 680 685
 Thr Val Lys Asn Glu Asn Val Gln Leu Val His Arg Phe Ser Asn Asp
 690 695 700
 Val Lys Thr Gly Glu Gly Asn Tyr Val Asp Phe Trp Ser Glu Leu Met
 705 710 715 720
 Pro Val Lys Asp Ser Phe Gln Lys Gly Asn Gly Pro Leu Lys Gln Phe
 725 730 735
 Gly Leu Gln Thr Ile Asn Gly Gln Gln Tyr Tyr Ile Asp Pro Thr Thr
 740 745 750
 Gly Gln Pro Arg Lys Asn Phe Leu Leu Gln Ser Gly Asn Asn Trp Ile
 755 760 765
 Tyr Phe Asp Ser Asp Thr Gly Val Gly Thr Asn Ala Leu Glu Leu Gln
 770 775 780
 Phe Ala Lys Gly Thr Val Ser Ser Asn Glu Gln Tyr Arg Asn Gly Asn
 785 790 795 800
 Ala Ala Tyr Ser Tyr Asp Asp Lys Ser Ile Glu Asn Val Asn Gly Tyr
 805 810 815
 Leu Thr Ala Asp Thr Trp Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly
 820 825 830
 Thr Thr Trp Thr Asp Ser Lys Glu Thr Asp Met Arg Pro Ile Leu Met
 835 840 845
 Val Trp Trp Pro Asn Thr Leu Thr Gln Ala Tyr Tyr Leu Asn Tyr Met
 850 855 860
 Lys Gln His Gly Asn Leu Leu Pro Ser Ala Leu Pro Phe Phe Asn Ala
 865 870 875 880
 Asp Ala Asp Pro Ala Glu Leu Asn His Tyr Ser Glu Ile Val Gln Gln
 885 890 895

Asn Ile Glu Lys Arg Ile Ser Glu Thr Gly Asn Thr Asp Trp Leu Arg
 900 905 910
 Thr Leu Met His Asp Phe Val Thr Asn Asn Pro Met Trp Asn Lys Asp
 915 920 925
 Ser Glu Asn Val Asn Phe Ser Gly Ile Gln Phe Gln Gly Gly Phe Leu
 930 935 940
 Lys Tyr Glu Asn Ser Asp Leu Thr Pro Tyr Ala Asn Ser Asp Tyr Arg
 945 950 955 960
 Leu Leu Gly Arg Met Pro Ile Asn Ile Lys Asp Gln Thr Tyr Arg Gly
 965 970 975
 Gln Glu Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val
 980 985 990
 Gln Ala Glu Gln Leu Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr
 995 1000 1005
 Ile Thr Ala Asn Asn Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp
 1010 1015 1020
 Ala Pro Asp Asn Ile Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr
 1025 1030 1035 1040
 Phe Asn Ala Ala Tyr Gly Met Asp Ser Asp Ala Val Ser Asn Lys His
 1045 1050 1055
 Ile Asn Ile Leu Glu Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn
 1060 1065 1070
 Lys Ile Gly Asn Pro Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser
 1075 1080 1085
 Leu Asn His Gly Leu Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala
 1090 1095 1100
 Ile Val His Gln Ser Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn
 1105 1110 1115 1120
 Val Val Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser
 1125 1130 1135
 Gln Asp Gln Ile Gln Asn Ala Ile Arg Asp Val Thr Gly Lys Asp Tyr
 1140 1145 1150
 His Thr Phe Thr Phe Glu Asp Glu Gln Lys Gly Ile Asp Ala Tyr Ile
 1155 1160 1165
 Gln Asp Gln Asn Ser Thr Val Lys Lys Tyr Asn Leu Tyr Asn Ile Pro
 1170 1175 1180
 Ala Ser Tyr Ala Ile Leu Leu Thr Asn Lys Asp Thr Ile Pro Arg Val
 1185 1190 1195 1200

Tyr Tyr Gly Asp Leu Tyr Thr Asp Gly Gly Gln Tyr Met Glu His Gln
 1205 1210 1215
 Thr Arg Tyr Tyr Asp Thr Leu Thr Asn Leu Leu Lys Ser Arg Val Lys
 1220 1225 1230
 Tyr Val Ala Gly Gly Gln Ser Met Gln Thr Met Ser Val Gly Gly Asn
 1235 1240 1245
 Asn Asn Ile Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala
 1250 1255 1260
 Thr Asp Thr Gly Thr Asp Glu Thr Arg Thr Gln Gly Ile Gly Val Val
 1265 1270 1275 1280
 Val Ser Asn Thr Pro Asn Leu Lys Leu Gly Val Asn Asp Lys Val Val
 1285 1290 1295
 Leu His Met Gly Ala Ala His Lys Asn Gln Gln Tyr Arg Ala Ala Val
 1300 1305 1310
 Leu Thr Thr Thr Asp Gly Val Ile Asn Tyr Thr Ser Asp Gln Gly Ala
 1315 1320 1325
 Pro Val Ala Met Thr Asp Glu Asn Gly Asp Leu Tyr Leu Ser Ser His
 1330 1335 1340
 Asn Leu Val Val Asn Gly Lys Glu Glu Ala Asp Thr Ala Val Gln Gly
 1345 1350 1355 1360
 Tyr Ala Asn Pro Asp Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val
 1365 1370 1375
 Gly Ala Ser Asp Asn Gln Asp Ala Arg Thr Ala Pro Ser Thr Glu Lys
 1380 1385 1390
 Asn Ser Gly Asn Ser Ala Tyr Arg Thr Asn Ala Ala Phe Asp Ser Asn
 1395 1400 1405
 Val Ile Phe Glu Ala Phe Ser Asn Phe Val Tyr Thr Pro Thr Lys Glu
 1410 1415 1420
 Ser Glu Arg Ala Asn Val Arg Ile Ala Gln Asn Ala Asp Phe Phe Ala
 1425 1430 1435 1440
 Ser Leu Gly Phe Thr Ser Phe Glu Met Ala Pro Gln Tyr Asn Ser Ser
 1445 1450 1455
 Lys Asp Arg Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe
 1460 1465 1470
 Thr Asp Arg Tyr Asp Leu Gly Met Ser Glu Pro Asn Lys Tyr Gly Thr
 1475 1480 1485
 Asp Glu Asp Leu Arg Asn Ala Ile Gln Ala Leu His Lys Ala Gly Leu
 1490 1495 1500

Gln Val Met Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly
 1505 1510 1515 1520
 Lys Glu Val Ala Thr Val Thr Arg Val Asp Asp Arg Gly Asn Val Trp
 1525 1530 1535
 Lys Asp Ala Ile Ile Asn Asn Asn Leu Tyr Val Val Asn Thr Ile Gly
 1540 1545 1550
 Gly Gly Glu Tyr Gln Lys Lys Tyr Gly Gly Ala Phe Leu Asp Lys Leu
 1555 1560 1565
 Gln Lys Leu Tyr Pro Glu Ile Phe Thr Lys Lys Gln Val Ser Thr Gly
 1570 1575 1580
 Val Ala Ile Asp Pro Ser Gln Lys Ile Thr Glu Trp Ser Ala Lys Tyr
 1585 1590 1595 1600
 Phe Asn Gly Thr Asn Ile Leu His Arg Gly Ser Gly Tyr Val Leu Lys
 1605 1610 1615
 Ala Asp Gly Gly Gln Tyr Tyr Asn Leu Gly Thr Thr Thr Lys Gln Phe
 1620 1625 1630
 Leu Pro Ile Gln Leu Thr Gly Glu Lys Lys Gln Gly Asn Glu Gly Phe
 1635 1640 1645
 Val Lys Gly Asn Asp Gly Asn Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn
 1650 1655 1660
 Met Val Lys Asn Thr Phe Ile Glu Asp Ser Val Gly Asn Trp Tyr Phe
 1665 1670 1675 1680
 Phe Asp Gln Asp Gly Lys Met Val Glu Asn Lys His Phe Val Asp Val
 1685 1690 1695
 Asp Ser Tyr Gly Glu Lys Gly Thr Tyr Phe Phe Leu Lys Asn Gly Val
 1700 1705 1710
 Ser Phe Arg Gly Gly Leu Val Gln Thr Asp Asn Gly Thr Tyr Tyr Phe
 1715 1720 1725
 Asp Asn Tyr Gly Lys Met Val Arg Asn Gln Thr Ile Asn Ala Gly Ala
 1730 1735 1740
 Met Ile Tyr Thr Leu Asp Glu Asn Gly Lys Leu Ile Lys Ala Ser Tyr
 1745 1750 1755 1760
 Asn Ser Asp Ala Glu Tyr Pro Thr Ser Thr Asp Val Gly Lys Met Leu
 1765 1770 1775
 Asp Gln Asn Lys Leu
 1780

<210> 3
 <211> 13

```
<400> 3
Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn Met Val Lys Asn
  1             5             10
```

```
<210> 4
<211> 13
<212> PRT
<213> Lactobacillus reuteri
```

```
<400> 4
Trp Tyr Phe Phe Asp Gln Asp Gly Lys Met Val Glu Asn
      1             5             10
```

```
<210> 5
<211> 13
<212> PRT
<213> Lactobacillus reuteri
```

<400> 5
Thr Tyr Tyr Phe Asp Asn Tyr Gly Lys Met Val Arg Asn
1 5 10

```
<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Primer

```
<220>  
<221> modified_base  
<222> (9)  
<223> a, t, c or g
```

```
<220>
<221> modified_base
<222> (15)
<223> a, t, c or g
```

```
<220>
<221> modified_base
<222> (18)
<223> a, t, c or g
```

```
<220>
<221> modified_base
<222> (21)
<223> a, t, c or g
```

<400> 6
qayaakwsna aksynrtngt nsargc

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (2)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (5)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (8)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (17)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

<400> 7
 gnkcncanat ratrcnctr na

22

<210> 8
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
 acaaccacca tggaattagg tcgcactgat gtaac

35

<210> 9
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9

gccagctgga tccgtcgact agtttatttt tgatcaagca tcttacc

47

<210> 10

<211> 545

<212> PRT

<213> Streptococcus mutans

<400> 10

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu
 1 5 10 15

Gln Leu Asn Trp Leu His Tyr Leu Met Asn Tyr Gly Ser Ile Val Ala
 20 25 30

Asn Asp Pro Glu Ala Asn Phe Asp Gly Val Arg Val Asp Ala Val Asp
 35 40 45

Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp Tyr Leu Lys Ala
 50 55 60

His Tyr Gly Val Asp Lys Ser Glu Lys Asn Ala Ile Asn His Leu Ser
 65 70 75 80

Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Gln Tyr Asn Lys Asp Thr
 85 90 95

Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg Leu Ser Leu Leu
 100 105 110

Tyr Ala Leu Thr Arg Pro Leu Glu Lys Asp Ala Ser Asn Lys Asn Glu
 115 120 125

Ile Arg Ser Gly Leu Glu Pro Val Ile Thr Asn Ser Leu Asn Asn Arg
 130 135 140

Ser Ala Glu Gly Lys Asn Ser Glu Arg Met Ala Asn Tyr Ile Phe Ile
 145 150 155 160

Arg Ala His Asp Ser Glu Val Gln Thr Val Ile Ala Lys Ile Ile Lys
 165 170 175

Ala Gln Ile Asn Pro Lys Thr Asp Gly Leu Thr Phe Thr Leu Asp Glu
 180 185 190

Leu Lys Gln Ala Phe Lys Ile Tyr Asn Glu Asp Met Arg Gln Ala Lys
 195 200 205

Lys Lys Tyr Thr Gln Ser Asn Ile Pro Thr Ala Tyr Ala Leu Met Leu
 210 215 220

Ser Asn Lys Asp Ser Ile Thr Arg Leu Tyr Tyr Gly Asp Met Tyr Ser
 225 230 235 240

Asp Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr Tyr Asp Ala Ile
 245 250 255

Asp Thr Leu Leu Lys Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Asp
 260 265 270
 Met Lys Ile Thr Tyr Val Glu Gly Asp Lys Ser His Met Asp Trp Asp
 275 280 285
 Tyr Thr Gly Val Leu Thr Ser Val Arg Tyr Gly Thr Gly Ala Asn Glu
 290 295 300
 Ala Thr Asp Gln Gly Ser Glu Ala Thr Lys Thr Gln Gly Met Ala Val
 305 310 315 320
 Ile Thr Ser Asn Asn Pro Ser Leu Lys Leu Asn Gln Asn Asp Lys Val
 325 330 335
 Ile Val Asn Met Gly Ala Ala His Lys Asn Gln Glu Tyr Arg Pro Leu
 340 345 350
 Leu Leu Thr Thr Lys Asp Gly Leu Thr Ser Tyr Thr Ser Asp Ala Ala
 355 360 365
 Ala Lys Ser Leu Tyr Arg Lys Thr Asn Asp Lys Gly Glu Leu Val Phe
 370 375 380
 Asp Ala Ser Asp Ile Gln Gly Leu Tyr Leu Asn Pro Gln Val Ser Gly
 385 390 395 400
 Leu Ala Val Trp Val Pro Val Gly Ala Ser Asp Asn Gln Asp Val Arg
 405 410 415
 Val Ala Ala Ser Asn Lys Ala Asn Ala Thr Gly Gln Val Tyr Glu Ser
 420 425 430
 Ser Ser Ala Leu Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe
 435 440 445
 Gln Asp Phe Val Thr Lys Asp Ser Asp Tyr Thr Asn Lys Lys Ile Ala
 450 455 460
 Gln Asn Val Gln Leu Phe Lys Ser Trp Gly Val Thr Ser Phe Glu Met
 465 470 475 480
 Ala Pro Gln Tyr Val Ser Ser Glu Asp Gly Ser Phe Leu Asp Ser Ile
 485 490 495
 Ile Gln Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Leu Ala Met Ser
 500 505 510
 Lys Asn Asn Lys Tyr Gly Ser Gln Gln Asp Met Ile Asn Ala Val Lys
 515 520 525
 Ala Leu His Lys Ser Gly Ile Gln Val Ile Ala Asp Trp Val Pro Asp
 530 535 540
 Gln
 545

<210> 11
 <211> 522
 <212> PRT
 <213> Leuconostoc mesenteroides

<400> 11

Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Val Val Val Glu Ala Glu
 1 5 10 15
 Gln Leu Asn Trp Leu Tyr Tyr Leu Met Asn Phe Gly Thr Ile Thr Ala
 20 25 30
 Asn Asp Ala Asp Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp
 35 40 45
 Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Ala Asp Tyr Phe Lys Leu
 50 55 60
 Ala Tyr Gly Val Asp Gln Asn Asp Ala Thr Ala Asn Gln His Leu Ser
 65 70 75 80
 Ile Leu Glu Asp Trp Ser His Asn Asp Pro Leu Tyr Val Thr Asp Gln
 85 90 95
 Gly Ser Asn Gln Leu Thr Met Asp Asp Tyr Val His Thr Gln Leu Ile
 100 105 110
 Trp Ser Leu Thr Lys Ser Ser Asp Ile Arg Gly Thr Met Gln Arg Phe
 115 120 125
 Val Asp Tyr Tyr Met Val Asp Arg Ser Asn Asp Ser Thr Glu Asn Glu
 130 135 140
 Ala Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Ser Glu Val Gln
 145 150 155 160
 Thr Val Ile Ala Gln Ile Val Ser Asp Leu Tyr Pro Asp Val Glu Asn
 165 170 175
 Ser Leu Ala Pro Thr Thr Glu Gln Leu Ala Ala Ala Phe Lys Val Tyr
 180 185 190
 Asn Glu Asp Glu Lys Leu Ala Asp Lys Lys Tyr Thr Gln Tyr Asn Met
 195 200 205
 Ala Ser Ala Tyr Ala Met Leu Leu Thr Asn Lys Asp Thr Val Pro Arg
 210 215 220
 Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln Tyr Met Ala Thr Lys
 225 230 235 240
 Ser Pro Tyr Tyr Asp Ala Ile Asn Thr Leu Leu Lys Ala Arg Val Gln
 245 250 255
 Tyr Val Ala Gly Gly Gln Ser Met Ser Val Asp Ser Asn Asp Val Leu
 260 265 270

Thr Ser Val Arg Tyr Gly Lys Asp Ala Met Thr Ala Ser Asp Thr Gly
275 280 285

Thr Ser Glu Thr Arg Thr Glu Gly Ile Gly Val Ile Val Ser Asn Asn
290 295 300

Ala Glu Leu Gln Leu Glu Asp Gly His Thr Val Thr Leu His Met Gly
305 310 315 320

Ala Ala His Lys Asn Gln Ala Tyr Arg Ala Leu Leu Ser Thr Thr Ala
325 330 335

Asp Gly Leu Ala Tyr Tyr Asp Thr Asp Glu Asn Ala Pro Val Ala Tyr
340 345 350

Thr Asp Ala Asn Gly Asp Leu Ile Phe Thr Asn Glu Ser Ile Tyr Gly
355 360 365

Val Gln Asn Pro Gln Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val
370 375 380

Gly Ala Gln Gln Asp Gln Asp Ala Arg Thr Ala Ser Asp Thr Thr Thr
385 390 395 400

Asn Thr Ser Asp Lys Val Phe His Ser Asn Ala Ala Leu Asp Ser Gln
405 410 415

Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Ala Phe Ala Thr Asp Ser
420 425 430

Ser Glu Tyr Thr Asn Val Val Ile Ala Gln Asn Ala Asp Gln Phe Lys
435 440 445

Gln Trp Gly Val Thr Ser Phe Gln Leu Ala Pro Gln Tyr Arg Ser Ser
450 455 460

Thr Asp Thr Ser Phe Leu Asp Ser Ile Ile Gln Asn Gly Tyr Ala Phe
465 470 475 480

Thr Asp Arg Tyr Asp Leu Gly Tyr Gly Thr Pro Thr Lys Tyr Gly Thr
485 490 495

Ala Asp Gln Leu Arg Asp Ala Ile Lys Ala Leu His Ala Ser Gly Ile
500 505 510

Gln Ala Ile Ala Asp Trp Val Pro Asp Gln
515 520

<210> 12

<211> 584

<212> PRT

<213> Leuconostoc mesenteroides

<400> 12

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Ile Val Gln Ala Glu
1 5 10 15

Gln Leu Asn Trp Leu His Tyr Leu Met Asn Phe Gly Ser Ile Thr Gly
 20 25 30
 Asn Asn Asp Asn Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp
 35 40 45
 Asn Val Asp Ala Asp Leu Leu Lys Ile Ala Gly Asp Tyr Phe Lys Ala
 50 55 60
 Leu Tyr Gly Thr Asp Lys Ser Asp Ala Asn Ala Asn Lys His Leu Ser
 65 70 75 80
 Ile Leu Glu Asp Trp Asn Gly Lys Asp Pro Gln Tyr Val Asn Gln Gln
 85 90 95
 Gly Asn Ala Gln Leu Thr Met Asp Tyr Thr Val Thr Ser Gln Phe Gly
 100 105 110
 Asn Ser Leu Thr His Gly Ala Asn Asn Arg Ser Asn Met Trp Tyr Phe
 115 120 125
 Leu Asp Thr Gly Tyr Tyr Leu Asn Gly Asp Leu Asn Lys Lys Ile Val
 130 135 140
 Asp Lys Asn Arg Pro Asn Ser Gly Thr Leu Val Asn Arg Ile Ala Asn
 145 150 155 160
 Ser Gly Asp Thr Lys Val Ile Pro Asn Tyr Ser Phe Val Arg Ala His
 165 170 175
 Asp Tyr Asp Ala Gln Asp Pro Ile Arg Lys Ala Met Ile Asp His Gly
 180 185 190
 Ile Ile Lys Asn Met Gln Asp Thr Phe Thr Phe Asp Gln Leu Ala Gln
 195 200 205
 Gly Met Glu Phe Tyr Tyr Lys Asp Gln Glu Asn Pro Ser Gly Phe Lys
 210 215 220
 Lys Tyr Asn Asp Tyr Asn Leu Pro Ser Ala Tyr Ala Met Leu Leu Thr
 225 230 235 240
 Asn Lys Asp Thr Val Pro Arg Val Tyr Tyr Gly Asp Met Tyr Leu Glu
 245 250 255
 Gly Gly Gln Tyr Met Glu Lys Gly Thr Ile Tyr Asn Pro Val Ile Ser
 260 265 270
 Ala Leu Leu Lys Ala Arg Ile Lys Tyr Val Ser Gly Gly Gln Thr Met
 275 280 285
 Ala Thr Asp Ser Ser Gly Lys Asp Leu Lys Asp Gly Glu Thr Asp Leu
 290 295 300
 Leu Thr Ser Val Arg Phe Gly Lys Gly Ile Met Thr Ser Asp Gln Thr
 305 310 315 320

Thr Thr Gln Asp Asn Ser Gln Asp Tyr Lys Asn Gln Gly Ile Gly Val
 325 330 335
 Ile Val Gly Asn Asn Pro Asp Leu Lys Leu Asn Asn Asp Lys Thr Ile
 340 345 350
 Thr Leu His Met Gly Lys Ala His Lys Asn Gln Leu Tyr Arg Ala Leu
 355 360 365
 Val Leu Ser Asn Asp Ser Gly Ile Asp Val Tyr Asp Ser Asp Asp Lys
 370 375 380
 Ala Pro Thr Leu Arg Thr Asn Asp Asn Gly Asp Leu Ile Phe His Lys
 385 390 395 400
 Thr Asn Thr Phe Val Lys Gln Asp Gly Thr Ile Ile Asn Tyr Glu Met
 405 410 415
 Lys Gly Ser Leu Asn Ala Leu Ile Ser Gly Tyr Leu Gly Val Trp Val
 420 425 430
 Pro Val Gly Ala Ser Asp Ser Gln Asp Ala Arg Thr Val Ala Thr Glu
 435 440 445
 Ser Ser Ser Ser Asn Asp Gly Ser Val Phe His Ser Asn Ala Ala Leu
 450 455 460
 Asp Ser Asn Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Ala Met Pro
 465 470 475 480
 Thr Ser Pro Glu Gln Ser Thr Asn Val Val Ile Ala Thr Lys Ala Asn
 485 490 495
 Leu Phe Lys Glu Leu Gly Ile Thr Ser Phe Glu Leu Ala Pro Gln Tyr
 500 505 510
 Arg Ser Ser Gly Asp Thr Asn Tyr Gly Gly Met Ser Phe Leu Asp Ser
 515 520 525
 Phe Leu Asn Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Leu Gly Phe
 530 535 540
 Asn Lys Ala Asp Gly Asn Pro Asn Pro Thr Lys Tyr Gly Thr Asp Gln
 545 550 555 560
 Asp Leu Arg Asn Ala Ile Glu Ala Leu His Lys Asn Gly Met Gln Ala
 565 570 575
 Ile Ala Asp Trp Val Pro Asp Gln
 580

<210> 13

<211> 535

<212> PRT

<213> Lactobacillus reuteri

<400> 13

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu
 1 5 10 15

Gln Leu Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr Ile Thr Ala
 20 25 30

Asn Asn Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp Ala Pro Asp
 35 40 45

Asn Ile Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr Phe Asn Ala
 50 55 60

Ala Tyr Gly Met Asp Ser Asp Ala Val Ser Asn Lys His Ile Asn Ile
 65 70 75 80

Leu Glu Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn Lys Ile Gly
 85 90 95

Asn Pro Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser Leu Asn His
 100 105 110

Gly Leu Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala Ile Val His
 115 120 125

Gln Ser Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn Val Val Ile
 130 135 140

Pro Asn Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser Gln Asp Gln
 145 150 155 160

Ile Gln Asn Ala Ile Arg Asp Val Thr Gly Lys Asp Tyr His Thr Phe
 165 170 175

Thr Phe Glu Asp Glu Gln Lys Gly Ile Asp Ala Tyr Ile Gln Asp Gln
 180 185 190

Asn Ser Thr Val Lys Lys Tyr Asn Leu Tyr Asn Ile Pro Ala Ser Tyr
 195 200 205

Ala Ile Leu Leu Thr Asn Lys Asp Thr Ile Pro Arg Val Tyr Tyr Gly
 210 215 220

Asp Leu Tyr Thr Asp Gly Gly Gln Tyr Met Glu His Gln Thr Arg Tyr
 225 230 235 240

Tyr Asp Thr Leu Thr Asn Leu Leu Lys Ser Arg Val Lys Tyr Val Ala
 245 250 255

Gly Gly Gln Ser Met Gln Thr Met Ser Val Gly Gly Asn Asn Asn Ile
 260 265 270

Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala Thr Asp Thr
 275 280 285

Gly Thr Asp Glu Thr Arg Thr Gln Gly Ile Gly Val Val Val Ser Asn
 290 295 300

Thr Pro Asn Leu Lys Leu Gly Val Asn Asp Lys Val Val Leu His Met
 305 310 315 320
 Gly Ala Ala His Lys Asn Gln Gln Tyr Arg Ala Ala Val Leu Thr Thr
 325 330 335
 Thr Asp Gly Val Ile Asn Tyr Thr Ser Asp Gln Gly Ala Pro Val Ala
 340 345 350
 Met Thr Asp Glu Asn Gly Asp Leu Tyr Leu Ser Ser His Asn Leu Val
 355 360 365
 Val Asn Gly Lys Glu Glu Ala Asp Thr Ala Val Gln Gly Tyr Ala Asn
 370 375 380
 Pro Asp Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser
 385 390 395 400
 Asp Asn Gln Asp Ala Arg Thr Ala Pro Ser Thr Glu Lys Asn Ser Gly
 405 410 415
 Asn Ser Ala Tyr Arg Thr Asn Ala Ala Phe Asp Ser Asn Val Ile Phe
 420 425 430
 Glu Ala Phe Ser Asn Phe Val Tyr Thr Pro Thr Lys Glu Ser Glu Arg
 435 440 445
 Ala Asn Val Arg Ile Ala Gln Asn Ala Asp Phe Phe Ala Ser Leu Gly
 450 455 460
 Phe Thr Ser Phe Glu Met Ala Pro Gln Tyr Asn Ser Ser Lys Asp Arg
 465 470 475 480
 Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe Thr Asp Arg
 485 490 495
 Tyr Asp Leu Gly Met Ser Glu Pro Asn Lys Tyr Gly Thr Asp Glu Asp
 500 505 510
 Leu Arg Asn Ala Ile Gln Ala Leu His Lys Ala Gly Leu Gln Val Met
 515 520 525
 Ala Asp Trp Val Pro Asp Gln
 530 535

<210> 14
 <211> 5
 <212> PRT
 <213> Neisseria polysaccharea

<400> 14
 Gln Trp Asp Leu Asn
 1 5

<210> 15
 <211> 10

<212> PRT
 <213> Neisseria polysaccharea

<400> 15
 Ile Val Arg Met Asp Ala Val Ala Phe Ile
 1 5 10

<210> 16
 <211> 4
 <212> PRT
 <213> Neisseria polysaccharea

<400> 16
 Phe Val Arg Ser
 1

<210> 17
 <211> 9
 <212> PRT
 <213> Neisseria polysaccharea

<400> 17
 Gly Leu Pro Arg Ile Tyr Leu Gly Asp
 1 5

<210> 18
 <211> 9
 <212> PRT
 <213> Neisseria polysaccharea

<400> 18
 Gly Leu Thr Tyr Leu His Leu Met Pro
 1 5

<210> 19
 <211> 6
 <212> PRT
 <213> Neisseria polysaccharea

<400> 19
 Asp Phe Ile Thr Asn His
 1 5